

Figure 1.

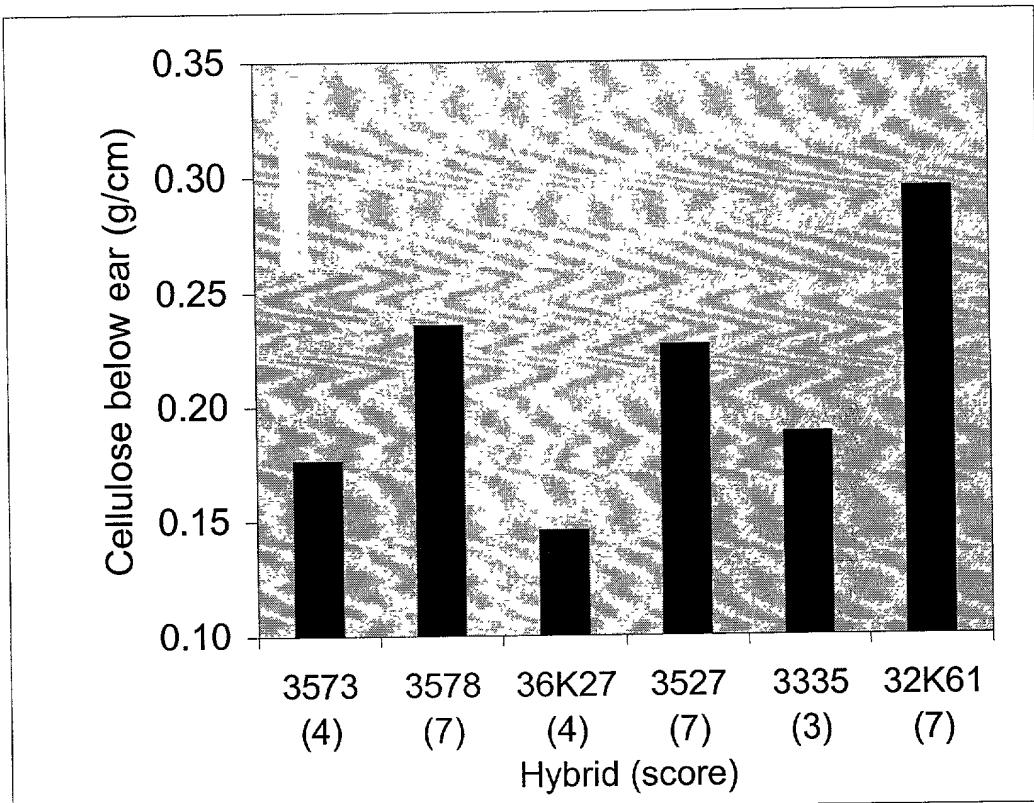


Figure 2

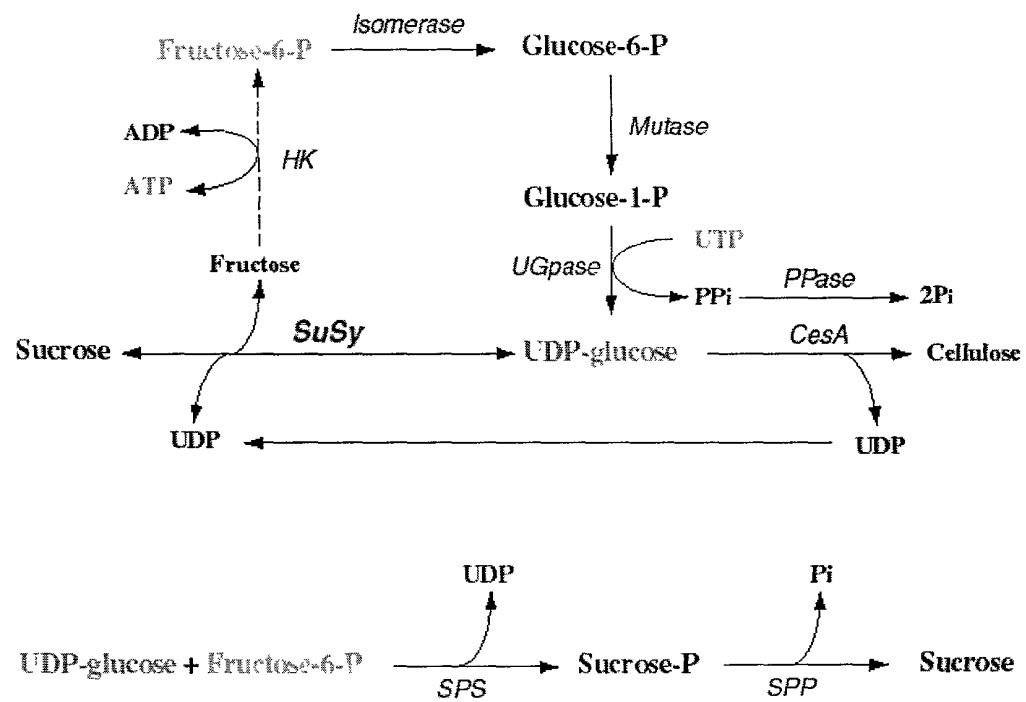


Figure 3.

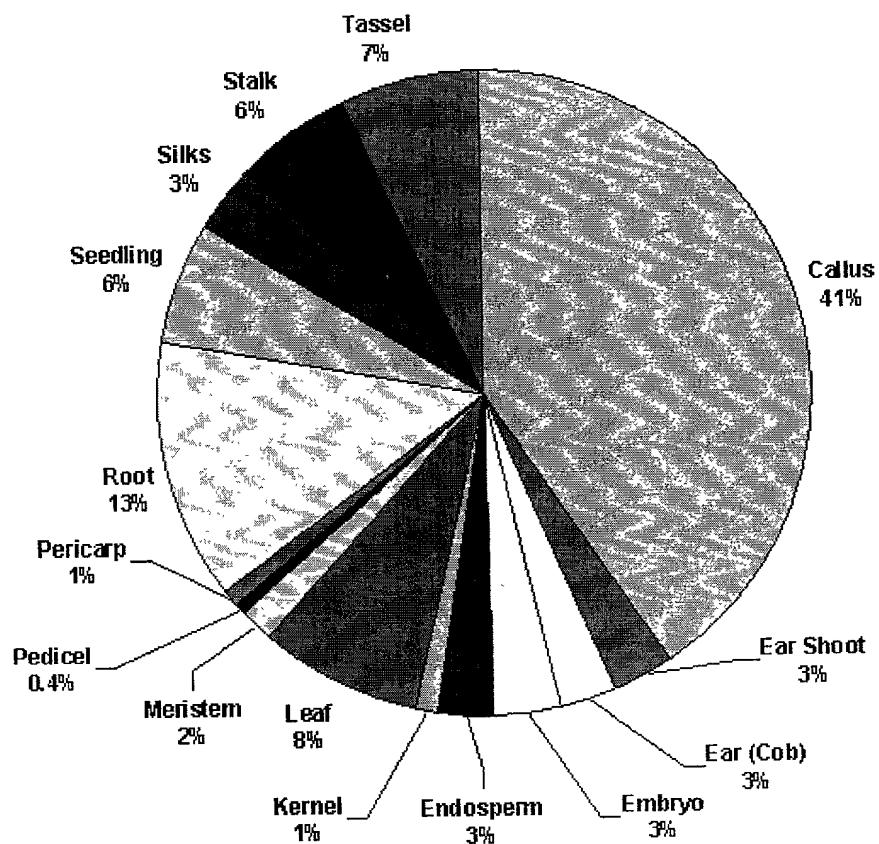


Figure 4.

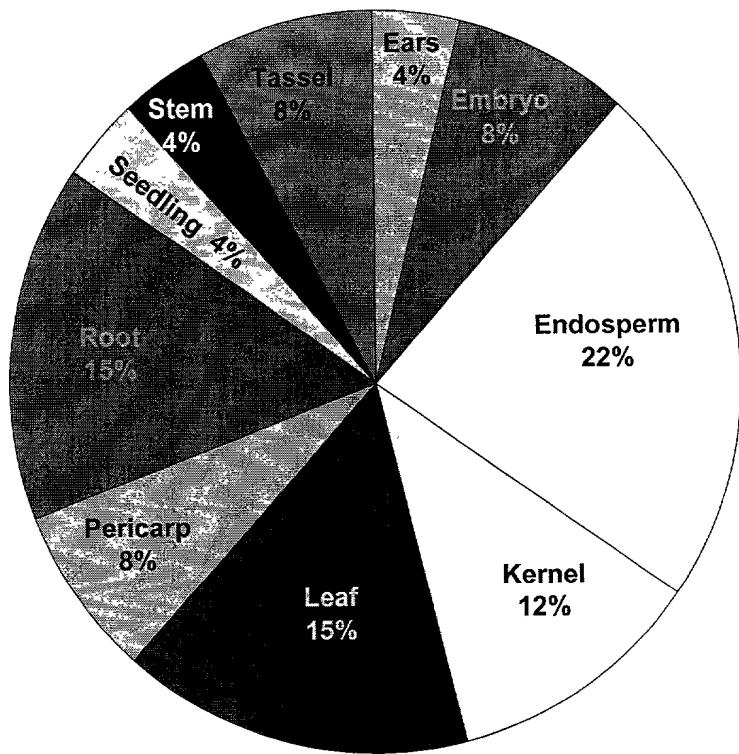


Figure 5

Allele 1: CACCCGG-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG



Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

	1	
Sh1	(1) -----MAAKLTRLHSLRERIGATFSHSPNELIALFSRYVHQKGMLQRHQ	
Sus1	(1) MGEGAGDRVLSRLHSVRERIGDLSAHPNELVAVETRLKNLGKGMLOPHQ	
Sus3	(1) -----STHASGRVEDTLHAHRNELLVALSKYVNKGILQPHH	
Consensus	(1) LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLOPHQ	
	51	
Sh1	(46) LLAEFD-AEFDSDKE -- KYAPFEDVLRAAQEAVLPPWVALAIRPRPGVM	
Sus1	(51) IIAEYNNAIPEAEEREKLKDGAEDVLRAAQEAVTPPWVALAIRPRPGVM	
Sus3	(40) ILDALDEVQGSGGRA-LAEGPFLDVRSQAQEAVLPPFVATAVRPRPGVM	
Consensus	(51) ILAEFD AI DADRE LKDPFEDVLRAAQEAVLPPWVALAIRPRPGVM	
	100	
Sh1	(93) DYVRVNSELAVEELSVSEYLAFKEQLVDGQMSNFVLEIDDEPFNASFP	
Sus1	(101) EYVRVNSELAVEELRVPEYLOKEOLVHEGPNNNFVLEIDDEPFNASFP	
Sus3	(89) EYVRVNSELVEQLTVSEYLREKEELVDGQHNDPYVLEIDDEPFNVVP	
Consensus	(101) EYVRVNSELAVEELSVSEYL FKEQLVDGQ N NFVLELDPEPFNASFP	
	150	
Sh1	(143) RPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLINELKAHNYKGTTMMLN	
Sus1	(151) RPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLINELRAHNYKGTMMLN	
Sus3	(139) RPNSRSSSIGNGVQFLNRHLSSIMERNRDCLEPLDFLRGRHKCHVMMEN	
Consensus	(151) RPSLSKSIGNGVQFLNRHLSSKLF DKESLYPLINFLRAHNYKG TMMLN	
	200	
Sh1	(193) DRIQSLRGLOSSERKAEEYLLSVPQDTPYSEEFNHRFOELGLEKGWGD TAK	
Sus1	(201) DRIRSTSALOGALRKAAEHTSTLQADTPYSEFHHRFOELGLEKGWGD TAK	
Sus3	(189) DRIQSLGRQSVLTKAEEHLSKLPADTPYSOFAYKFOEWGLEKGWGD TAK	
Consensus	(201) DRIQSL ALQSALRKAAEHLSSL PADTPYSEF HRFOELGLEKGWGD TAK	
	250	
Sh1	(243) RVLDTLHLLLEAPDPANLEKFLGTIPMMENVILSPHGYFAQSNVLG	
Sus1	(251) RAQETIHLLLLEAPDPSTLEKFLGTIPMVENVILSPHGYFAQANVLG	
Sus3	(239) HVLEMILHLLDIIQAPDPSTLEKFLGTIPMMENVVSPHGYFAQANVLG	
Consensus	(251) RVLETIHLLLLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG	
	300	
Sh1	(293) YPDTCGGQVYYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLDACT	
Sus1	(301) YPDTCGGQVYYILDQVRALENEMLLRIKQCGLDITPKILIVTRLLPDATGT	
Sus3	(289) LPDTGGQVYYILDQVRALENEMVRLKKQGLDITPKILIVTRLLPDATGT	
Consensus	(301) YPDTCGGQVYYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDATGT	
	350	
Sh1	(343) TCGQRLEKVGTTEHTDILRVLPFRNENGILRKWISRFDVWVYLETYTEDVS	
Sus1	(351) TCGQRLEKVIGTEHCHILRVLPFRNENGILRKWISRFDVWVYLETYTDVA	
Sus3	(339) SGNQRIERISGTOHTYILRVLPFRNENGILKKWISRFDVWVYLETFAEDAA	
Consensus	(351) TCGQRLEKVIGTEHCHILRVLPFRNENGILRKWISRFDVWVYLETYTEDVA	
	400	
Sh1	(393) SEIMKEMQAKPDLLIGNYSDGNLVATIAHKLGVTQCTIAHALEKTKYPN	
Sus1	(401) HETAGELQANPDLLIGNYSDGNLVATIAHKMGCVTHGTIAHALEKTKYPN	
Sus3	(389) GETAAELOQTPDLIGNYSDGNLVASLISYKMGVQCTIAHALEKTKYPD	
Consensus	(401) EIAAELOQTPDLIGNYSDGNLVASLLAHKGVTQCTIAHALEKTKYPN	
	450	
Sh1	(443) SDIYLDKEDSQYHESCOFTADLIAMNHTDITSTFQEIAGSKDTVGQYE	
Sus1	(451) SDIYWKKFEDHYHESCOFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE	
Sus3	(439) SDIFWKFDKEKYHESCOFTADLIAMNADFIITSTFQEIAGSKNTVGOYE	
Consensus	(451) SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE	
	500	
Sh1	(493) SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMMSVYYPYIETDKRLTAFH	
Sus1	(501) SHIAFTMPGGLYRVVHGIDVFDPKFNIVSPGADMISIYFPYTESHKRLTSLH	
Sus3	(489) SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMISIYFPHTEKAKRITSLH	
Consensus	(501) SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMISIYFPYTES KRLTSIH	

Figure 8a

	551	600
Sh1	(543) PEIEELIYS DVENSEHKFVL KDKKKPTIESMARLDRVKNMTGLVEMYGKN	
Sus1	(551) PETBELLIS SQTENTEHKFVL NDRNKP TIESMARLDRVKNLTGLVELYGRN	
Sus3	(539) GSTENLIYDPEQND EHIGHLDORSKPILESMARLDRVKNITGLVAFAKC	
Consensus	(551) PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN	
	601	650
Sh1	(593) ARIREL VNL VVAGDHGK - ESKDRE EQAEFKKMYSL IDEYKLKGHIRWIS	
Sus1	(601) KRIQEL VNL VVAGDHGK - P SKDKEE QAEFKKMFDLIEQYNLN GHIRWIS	
Sus3	(589) ARIREL VNL VVAGYNDVNKS KDR EIAEIEKMHBLKTHNLFCQFRWIS	
Consensus	(601) ARIREL VNL VVAGDHG SKDRE EQAEFKKMHDLID YNL GHIRWIS	
	651	700
Sh1	(642) AQMNRVRNGELYRYICDTKGAFVQPAFYEARGLTVESMTGCLPTIATC H	
Sus1	(650) AQMNRVRNGELYRYICDTKGAFVQPAFYEARGLTVESMTGCLPTFATAY	
Sus3	(639) AQMNRVRNGELYRYICDTKGAFVQPAFYEARGLTVESMTGCLPTFATLH	
Consensus	(651) AQMNRVRNGELYRYICDTKGAFVQPAFYEARGLTVESMTGCLPTFAT H	
	701	750
Sh1	(692) GGPAAEIIVDGVSGLHTDPYHSDKAADILVNFFDKCKADPSYWDEISQGGL	
Sus1	(700) GGPAAEIIVHGVSGLHTDPYQGDKA SALLVDEFPDKCQAE SHUSKISQGGL	
Sus3	(689) GGPAAEIIEHGVSGLHTDPYHPEQAVNLMADEPDRCKQDPDHWNLSGACH	
Consensus	(701) GGPAAEIIVHGVSGLHTDPYH DKAA LLVDFFDKCKADPSHW ISQGGL	
	751	800
Sh1	(742) QRIFYEKYTWKLYSERLMLTGIVYGFNKIVSNLERRET RRYLEM FYALKYR	
Sus1	(750) ORTEEKYTWKLYSERLMLTGIVYGFNKIVSNLERRET RRYLEM FYALKYR	
Sus3	(739) ORTYEKYTWKLYSERLMLTGIVYGFNKIVSNLERRET RRYLEM FYALKYR	
Consensus	(751) QRIFYEKYTWKLYSERLMLTGIVYGFNKIVSNLERRET RRYLEM FYALKYR	
	801	817
Sh1	(792) SLASQVPLSF-----	
Sus1	(800) DMASTVPLAVEGEPESSK	
Sus3	(789) ELAKTVPLAID-QPQ--	
Consensus	(801) SLASTVPLAID P	

Figure 8b

50

Sh1	(1)	AAACCCTCCCTCCCTCCATTG	GACTGCTTGC	TCCGTGACCATTTG
Sus1	(1)	-	-	GCCTGAG-GATCCAGGAAGAGG
Sus3	(1)	-	-	CAC
Consensus	(1)		G CTG	G TCC G GA A G

100

Sh1	(51)	GGTATTCTGAACCATCGAGCCATGGCTGCCAAGCTGACT	CGGCCCTTCAGAG	
Sus1	(26)	CA-ATGGGGAAAGGTGCAGGTGACCGTGTC	-CTGAGCCGCCCTCCACAG	
Sus3	(1)	-	CTCGAC-CCACGC	
Consensus	(51)	AT G A T AG	TG C	CTGAGTCGCCCTCCACAG

150

Sh1	(101)	TCTTCGGCAACCGCTTGGT	GCCACCTCTCCTCCC	ATGCCAATGAACTGA
Sus1	(72)	CGTCAGGGAGCGGA	ATGGCACTCAC	CTCTGCCCACCCCAATGACCTTG
Sus3	(13)	GTCCGGCGACGCCG	CTGAGGACACCGCTCCACCGCG	ACCGCAACGAGCCTG
Consensus	(101)	TC GCGA CGC TTGG	GACACCCCTCTCCGCC	ACCCCAATGAGCT G

200

Sh1	(151)	TACCACTCTTTC	CAGCTATGTT	ACCACGGCAAGGAA
Sus1	(122)	TCCCGCTCTTC	ACCCAGGCTGAAA	ACCGTATGCTGCCAGCC
Sus3	(63)	GGCCCTCTCTG	CCAATACGT	ACAAGGGGAAAGGCATCC
Consensus	(151)	TCGCCCTCTT	TCCAGGTA GT	AACCAGGG AAGGG ATGCTGCCAGCCC

250

Sh1	(201)	CATCAGCTGCTTCCG	CAAGTTTGA	--TGC	--CCTGTT	--TGATA	TGAA
Sus1	(172)	CACCAAGATCA	TTCCC	ACTACAACA	ATGCGATCCCTGAGG	CTGAGGCC	
Sus3	(113)	CACCAACATCC	TCGACCG	CTCGACCGAGT	--CCACGG	CTCCGGGGCC	
Consensus	(201)	CACCAAGATCC	TGCGAGTTGAC	ATGC	CCTG G	CTGAG G	GA

300

Sh1	(242)	CAACGAGAAG	--TATG	ACCAATTGAA	GATTC	TTCTTC	CGTGC	TCTCAGGA
Sus1	(222)	GAGCTCAAG	-GATCTG	GTCTT	TGAG	ATCTCCTG	AGGGCAGCT	CGTACAGGA
Sus3	(158)	CGCCCGGT	ATGCC	CGGAGCT	CTTCCTCGACGTG	CTCC	CGGCCAGGA	
Consensus	(251)	CAAGC CAAG	GATGGACC	TTTGA	GACGT	CG	GC	GCTCAGGA

350

Sh1	(290)	ACCAATTGCT	CCCCCA	ATGGGTTG	CACTT	TCTAT	CAGGCCAAGGG	CTG
Sus1	(270)	GGCGATTCTCA	ATCCCCC	CATGGGTT	CCACTTG	CCAT	CCCCCT	TASCCCTG
Sus3	(208)	GGEGATCTG	GGG	GGT	TCG	GGCAT	CCGGG	GGCCCCGG
Consensus	(301)	GGCGATTGTG	CTCCCCC	CATGGGTTG	CACTTG	GC	CCCC	AGGCCTG

400

Sh1	(340)	GTGCTGGCATT	TACAT	TCGGG	TGAA	TGTAAGT	GACCTGG	GTGCAAGGAG
Sus1	(320)	GTGCTGGCAGT	ATG	TGACG	GTCAAC	GTCACTG	AGCTGG	TGAGGAG
Sus3	(258)	GAGTTGCG	ACTACG	TCCGCG	CGCAAC	CTTACCG	AGCTGAGC	CTCCACCAAG
Consensus	(351)	GTGTCTGG	GAGTACGT	CGGGT	CAACGT	AGTGAG	CTCGCTGT	GAGGAG

450

Sh1	(390)	CTCACTGTTCTG	AGTACTT	GGCATTCA	AGGAACAC	CTGCTGG	GTGCAAGG	AG
Sus1	(370)	CTGAGACTTCTG	AGTACTG	GGCATTCA	AGGAACAC	GTGCTGG	CAAGAAGG	
Sus3	(308)	CTCACACTCTG	GGAGTACCG	CTGCTGG	AGGAGGAG	CTTGTG	CCGCCA	
Consensus	(401)	CTGAGAGTTCTG	GAGTACCTG	CTG	TTCAAGGAACAG	CTTG	GGGA	GGACA

500

Sh1	(440)	ATCCAACAGCAAC	TTTGTG	CTGAGCTG	TGATTT	TGACCC	CTTCAAT	CGCT
Sus1	(420)	CCCAAACAGCAAC	TTTGTG	AGCTGG	GTGAC	CCATTCA	ATCGCT	
Sus3	(358)	GGAAATGATCCC	TA	CGCTTGAG	CTTGACTT	CGAGCCG	TTG	CAATGTCT
Consensus	(451)	CCCAACAA	ACAAC	TTTGTG	TTGAGCTT	GTGAGCC	TTCAAT	GCCT

550

Sh1	(490)	CGTTCTGG	CTTCC	TCATG	TGCAAGT	CCATCGGAA	ATGG	GTGCAATTC
Sus1	(470)	CGTTCTCC	CCG	CTTCTG	TGCAAGT	CCATGG	CAATGG	CGTCCAGTTC
Sus3	(408)	CAGCCCC	ACG	CCCAA	ATCCG	TACAT	TATGG	AAACGCTG
Consensus	(501)	CTTCCC	CGT	CTTCTG	CAAAGT	CCATTGG	AAATGG	GTGAGTTC

Figure 9a

		551	
Sh1	(540)	CTTAACCGACACCTGCGGTCCAAGTTGTTCCAGGACAAGGAGAGTTCTA	600
Sus1	(520)	CTCAACAGGCACCTGTCATCAAAGCTTCTCCATGACAAGGAGAGCACTA	
Sus3	(458)	CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTCTTGGA	
Consensus	(551)	CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA	
		601	
Sh1	(590)	CCCCCTTGCTGAACCTCTGAAGGCTCATAACTACAACGGCACGACCATGA	650
Sus1	(570)	CCCCCTTGCTCAACTCTCTCCGCCAACAACTACAACGGGATGACCATGA	
Sus3	(508)	CCCCCTGTTGGATTTCCTCCGTGGCACCAGGGACAAGGGGATGTTATCA	
Consensus	(601)	CCCCCTTGCTGAACCTCTCCG GCCCACAACATAAGGGGA GAC ATGA	
		651	
Sh1	(640)	TCTTGAATGACAGAACATCCAAGGCCTCGTGTCTCCAAATGATCCCTGAGA	700
Sus1	(620)	TCTTGAACGACAGAACATGCCAGTCACTGCTCTGCAAGTGGGCTGAGG	
Sus3	(558)	TGCTTAATGATAGATAAAGCTGGGAGGCTTAGTCTGTGCTGACC	
Consensus	(651)	TGTTGAATGACAGAACATCCAAGGCCT GTGGTCT CAATCTGCGCTGAG	
		701	
Sh1	(690)	AAGGGAGAGGAGCTATCTACTGAGTGTCTCAAGACACCTGGCTACTGGGA	750
Sus1	(670)	AAGGGAGAGGAGCACCGTGTCACCCCTACAAGCTGATACCCATACTCTA	
Sus3	(608)	AAGGGAGAGGAGCACCTGTCAAGACTCCCTGCTGACACACCAACTCACA	
Consensus	(701)	AAGGCTGAGGGAGCACCTGTC A CT CCTGTCGACAC CCATACTC GA	
		751	
Sh1	(740)	GTTCAACCATAGGTTCCAAGAGCTTGGCTTGAGAAGGTTGGGTCACA	800
Sus1	(720)	ATTTCAACCACAGGTTCCAGGAACCTTGGCTTGAGAAGGTTGGGCTGATT	
Sus3	(658)	ATTTGCTTATAAAATTCAAGAGTGGGGCTGGAGAACCTTGGGCTGATA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCTGGAGAAGGGTTGGGGTGATA	
		801	
Sh1	(790)	CTGGGAAGCTGTTCTCGACACACTGGACTTCTGACCTTCTTGAG	850
Sus1	(770)	GGGCTAAGGGGTCACAGGAGACTATACCCCTCTCTGACCTCTGGAG	
Sus3	(708)	CAGCAGGACATTTGGAAATGATCATCTCTCTCTAGACATCATCAG	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCTTCT GACCTCTTGAG	
		851	
Sh1	(840)	CCCCCTGATCTGCCAACTTGGACAACTTCCCTGGAACTATAACCAATGAT	900
Sus1	(820)	CCCCCAGATCCGTCACCCCTCGAGAGAACTTCCCTGGAAACGATCCCCATGGI	
Sus3	(758)	GGGCGAGACCCATCTACCCCTAGAGAAATCTTGGGAGGAACTGGATGAT	
Consensus	(851)	CCCCCAGATCC TCCACCCCTGGAGAAGTTCCTTGGAAACGATCCCCATGAT	
		901	
Sh1	(890)	CTTCAACCTTGTATCTGTCCTCATGGCTACTTCCCTTCAAGCTTCAAC	950
Sus1	(870)	CTTCAATGTCGTATGCTCTCCCTCATGGT TACTTTCGCTCAAGCTTAA	
Sus3	(808)	TTTTAACCTTGTGTGGTATCCCCCTATGGATACTTITGGCTCAAGCTTAA	
Consensus	(901)	GTTCAACGTTGTATCCT TCCCTCATGG TACTTCGCTCAAGCTTAA	
		951	
Sh1	(940)	TGGCTTGGAAACCCCTCACACTGGCGCTCAAGCTTGTGTACATCTGGATCAA	1000
Sus1	(920)	TCTGGCTTACCCCTGACACCGGAGGCCAGGTGTCTCTACATCTGGATCAA	
Sus3	(858)	TATTAAGCTTGGCAGACACAGAGGACAGATCTCTATATACTGGACCAA	
Consensus	(951)	T TT GG TACCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA	
		1001	
Sh1	(990)	GTCCCCGGCTTGGAGAACATGAGTGTCTGAGGGATTAAGCAGCAAGGCT	1050
Sus1	(970)	CTGGGGCCCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT	
Sus3	(908)	GTCCCCGGCACTACAAAAATGAGATGGTTCTCCCTTAAAGAAAACAAGGGCT	
Consensus	(1001)	GTCCGTGCT TGGAGAACATGAGTGTCTGAGGGAT AAGCAGCAAGG CT	
		1051	
Sh1	(1040)	CGATATCACCTCCGAAGATGCTCATTTGTTACCAAGGCTGTTGCCTGAGGCTG	1100
Sus1	(1020)	CGACATCACGGGGAAAGATCCCTATTTCTACAGGAGGTGCTCCCTGAGGCAA	
Sus3	(958)	CGATGTTCCCGAACGATTTCTCATTTGTTACTCGGCTGATACCAGATGCAA	
Consensus	(1051)	TGATATCAC CGGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA	

Figure 9b

40030414029402

		1101		1150
Sh1	(1090)	CTGGCACTACGTGCCGTAGCGCTGCAGAAGGTCAITGGTACTGAGCAG		
Sus1	(1070)	CTGGCACCACTGTGCCCTAGAGGCTTGAGAAGTCCTTGGCACCGAGCAC		
Sus3	(1008)	AAGGAACATCATGCAATCAGGGCTTGAGAGAAATTAGTGAACACAGCAT		
Consensus	(1101)	CTGG AC AC TGCGGTAGCGGCTTGAGAAGGTCAATTGG AC GAGCAC		
		1151		1200
Sh1	(1140)	ACAGAACATCAATTGGCTTCCCTTCAGAAATGAGAATGGCATCCTCCGCAA		
Sus1	(1120)	TGCCATATCCCTGGCGATGCCATTCAAGAACAGAAAACGGAATCGTTGGCAA		
Sus3	(1058)	ACTTACATATTAAUGACCTCCCTTCAGAAATGAAAATGGAACTTAAGAA		
Consensus	(1151)	AC ACATC TTGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA		
		1201		1250
Sh1	(1190)	GIGGATOTCTCGTTTTCATGCTGGCCATACCTGGAGACATAACACTGAGG		
Sus1	(1170)	GIGGATCTGGCAATTTCAGACTGGCGTACCTGGAGACTTACACTGATG		
Sus3	(1108)	ATGGATATCAACATTTGATGTGEGGCCATATCTGGAAACATTGCTGAGG		
Consensus	(1201)	GTGGATCTC CGATTGATGTCTGCCATACCTGGAGACATAACACTGAGG		
		1251		1300
Sh1	(1240)	ATGTTTCCACTGAAATAATGAAACAAATGCCAGGGCAAGCTGACCTTATC		
Sus1	(1220)	ACCTGGGGCATCAGATGCTGGAGAGCTTCAGGCCATCCTGACCTGATC		
Sus3	(1158)	ATGCTCTGGTCAAATTGCTGCTCAATTACAAGGTAACACTCAGACTTCATA		
Consensus	(1251)	ATGTTGC GTGAAATTGCTG AGAA T CAGGCCATCCTGACCT ATC		
		1301		1350
Sh1	(1290)	ATTGCCAAACTACAGGCAATGGCAACCTACTCGGCACTCTGCTGGGCCACAA		
Sus1	(1270)	ATCGGAAACTACAGCTGACGCCAACCTTCTGCTGGTCTGGCCACAA		
Sus3	(1208)	ATTGCCAAACTACAGTGTGAAATCTTCTGCTGGTCAATTGCTATCTAACAA		
Consensus	(1301)	ATTGGAAACTACAGTGTGAAACCTTGT GCGTCTTGCTCGC CACAA		
		1351		1400
Sh1	(1340)	GTTGGGAGTCACTCACTGTACCATCGCTCATGCCCTGGAGAAAACCAAAAT		
Sus1	(1320)	GATGGGTCTTACTCACTGTACCATGCCCTGGCTTGAGAAAACAAACTAAGT		
Sus3	(1258)	GATGCCAAATTACCAAGTGCACATGCCATGCTCTGCCAACAGACTAAGT		
Consensus	(1351)	GATGGGAGTTACTCAGTGTACCATGCTCATGC CTGGAGAAAACAAACTAAGT		
		1401		1450
Sh1	(1390)	ACCCCAACTGGACATCTACTTGACAAATTGGACAGCCACTACCAACTTC		
Sus1	(1370)	ACCCGAACTCCACCTGACTGGACAAAGTTGAGGATCACTACCACTTC		
Sus3	(1308)	ATCCAGATTCAAGATATTGGAGAATTCCATGAGAAGTACATTTC		
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC		
		1451		1500
Sh1	(1440)	CTCTGGCAACTCACAGCTGACCTATTGCCATGAAACCACCGATTTCAT		
Sus1	(1420)	CTGGTGGCAACTCACCACTGACTTTGATTCATGAAACCACCGACTTCAT		
Sus3	(1358)	TCTCTGGCAACTCACGCTGCTATAATTGCTATGAAACATGCTGATTTAT		
Consensus	(1451)	TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCATTTCAT		
		1501		1550
Sh1	(1490)	CATCACCAACACATTCAACAAATGCCAGCAAGGACACCCCTGGGC		
Sus1	(1470)	CATCACCAACTTCAACAGCAAGGCCAACAGAGGACACCGTGGCC		
Sus3	(1408)	CATCACCAACACATACGAAAGATGCTGAAAGGAAATAACTGTGGAC		
Consensus	(1501)	CATCACCAACGACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C		
		1551		1600
Sh1	(1540)	AGTACGGAGTCATATCCGTTCACTCTTCTGGCTCTACCGTGTCTC		
Sus1	(1520)	AGTACGGAGTCACACATGGCTCACAAAGCTCCCTGCTACCGCGTGTCTC		
Sus3	(1458)	AGTACATGAGTCATACTGCCCTTACTCTGCCCTGGCTCTGACCGAGTTGTC		
Consensus	(1551)	AGTACGAGTC CATAT GCGTTCACTCTGCCCTGG CTGTACCG GTTGTC		
		1601		1650
Sh1	(1590)	CATGGCATCGATGTTCGATGCCAAAGTTCAACATTCCTCTGCTGGAGC		
Sus1	(1570)	CACGGGATTCATGCTGGACCCCAAGTTCAACATTCGTTCTCTGGCGC		
Sus3	(1508)	CATGGGATCCATGCTGGACATCAAAAGTTCAATATACTCTCTCTGGAGC		
Consensus	(1601)	CATGGCATCGATGT TTGATGCCAAAGTTCAACAT GTCTCTCTGGAGC		

Figure 9c

		1651		1700
Sh1	(1640)	AGACATGAGTGTACTACCGTTATACGGAAACGACAAGAGACTCACTG		
Sus1	(1620)	GAACCTGTCCATCTACTTCCCGTACACGGACTCGCACAAGAGGCTGACCT		
Sus3	(1558)	TGACATGTCCATACTTCCGACTACCCGAGAAGGCCAACGCACTCACCT		
Consensus	(1651)	GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT		
		1701		1750
Sh1	(1690)	CCTTCGATCTGAAAATCGAGGAGCTCATCTACAGGGACGTCGAGAACCTC		
Sus1	(1670)	CCCTTCACCCGGAGATGAGGAGCTCTGTACAGCCAAACCGGAGAACAGG		
Sus3	(1608)	CTCTTGATGGTCAATCGAAAATTGATTAATGACCCGGAGCAAAACGAT		
Consensus	(1701)	CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C		
		1751		1800
Sh1	(1740)	GAGGCACAAGTTGGTGTGAAGGACAACAAGAAGCCGATCATCTTCTGGAT		
Sus1	(1720)	GAGGCACAAGTTGGTGTGAACCAACACAAGCCAAATCATCTTCTGGAT		
Sus3	(1658)	GAACACATTGGGCATCTGGATCACCGGTCAAAGCCCACATCCTCTCTCCAT		
Consensus	(1751)	GAGGCACAAGTTGGTGTGAACAGGAA AAGCC ATCATCTTCTCCAT		
		1801		1850
Sh1	(1790)	GGGGCGCTCTGACCCCCGTGAAGAACATGACAGGGCTGGTGTGAGATGACG		
Sus1	(1770)	GGCTCGCTCTGACCCCCGTGAAGAACATGACAGGGCTGGTGTGAGATGACG		
Sus3	(1708)	GGCAAGACTCCACAGGTGAACAAACATAAACAGGGCTGGTGTGAGCTTTG		
Consensus	(1801)	GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTGTGAG TGACG		
		1851		1900
Sh1	(1840)	GCAAGAACCGGGCCCTCACGGACCTGGCAACCTCTGTATCGTTGCCGGT		
Sus1	(1820)	GGCGGAACAAGGGGCTCCAGGAGGTGGTGAACCTCTCTGCGCTCTGCCGGC		
Sus3	(1758)	CTAAGTGCCTAAGCTGAGGGAGCTGGTAAACCTCTCTGCGCTTGCCTGGG		
Consensus	(1851)	GCAAGAACCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTGTGCCGG		
		1901		1950
Sh1	(1890)	GACACCGG---CAAGGAGTCAAGGACAGGGACACCACCGGGAGTCAA		
Sus1	(1870)	GACCATGG---CAACCTTTCGAACCAACAGGAGGACAGGCCGAGTCAA		
Sus3	(1808)	TACATGTGTCAACAAGTCCAAGAACAGGAAATCGGGAGATAGA		
Consensus	(1901)	GACCATGG CAAC AGTCCAAGGACAGGGAGGAGCAGGCGAGTCAA		
		1951		2000
Sh1	(1937)	GAAGATGTACAGCCTCTCGACGAGTACAAGTTGAAGGCCATATCCGGT		
Sus1	(1917)	GAAGATGTTGACCTCATCGACAGCTACAACTGAACGGGACATCGGCT		
Sus3	(1858)	GAAGATGATGAACCTCATGACAGGAAACAAACTCTGCGGAGTGGCT		
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACCTGAACGGCA ATCCGCT		
		2001		2050
Sh1	(1987)	GGATCTGGGGAGATGAACCTGTCCCCAACGGGAGCTGTACCGCTAC		
Sus1	(1967)	GGATCTCCCCAGATGAACCTGTGCTCAACGGGAGCTGTACCGCTAC		
Sus3	(1908)	GGATCTCTGCCAGACAAACAGGCCGCTAACGGGAGCTATGGCTAC		
Consensus	(2001)	GGATCTC GCCCAGATGAACCG GTCCGCAACGGCAGCTGTACCGCTAC		
		2051		2100
Sh1	(2037)	ATTTGGGATAACCAAGGGGCTTCGTGAGGCTGGCTTCTACGAAGCGTT		
Sus1	(2017)	ATCTGGGACACCAAGGGGCTTCTCTGAGGCTCTCTACGAGGGTTT		
Sus3	(1958)	AATGGCTGATACCCATCTGCTTCTGAGGCTGGCTTCTACGAGGGTT		
Consensus	(2051)	ATCTGGGATACCAAGGGCGC TTCTGAGGCTGC TTCTACGAAGCGTT		
		2101		2150
Sh1	(2087)	CGGGCTGAGCTGATCCAGTCCATGACGTGGGGCTGGCAACGATGCGCA		
Sus1	(2067)	CGGGGGAGGGTGTGAGGCCAACCTGGGGCTGGCAACGATGCGCA		
Sus3	(2008)	CGGGTCTACCCCTGCTGAGGCCAACCTGGGGCTGGCAACGATGCGCA		
Consensus	(2101)	CGG CTGAC GTGGTGGAGGCCATGACCTGCCTGCGG CTGCC ACGTTCGCGA		
		2151		2200
Sh1	(2137)	CCTGCCATGGGGCCCTGAGGATCATGCTGGAGGGGTAATCTGGCTG		
Sus1	(2117)	CGGCCTACGGGGCTCCGCGGAGATCATGCTGGAGGGGCTGCTGGCTAC		
Sus3	(2058)	CGCTCCATGGAGGCTCAGCTGAGGATGATAAGGATCTGGCTGGGCTTC		
Consensus	(2151)	CC CCATGGCGGTCC GCTGAGGATCATCGTGCACGGCGT TCTGGCTTC		

Figure 9d

			2201
Sh1	(2187)	CACATTGACCCTTACCAACAGGCCACAACCCCCGGGGATAATCTGGTCAACTT	
Sus1	(2167)	CACATCGACCCTTACCAAGGGGACAACCCGTCGGCCCTCTCTGGACTT	
Sus3	(2108)	CACATTGACCCTTACCAACAGGCCACAACCCCCGTGTTAACTGATGCCGACTT	
Consensus	(2201)	CACATTGACCCTTACCAACAGGCCACAACCCCCGGGGATATCTGGTCAACTT	
			2251
Sh1	(2237)	CTTCACAAAATGCAAGCCAGATCCGAGCTACTCGGACCGACATCTCACAGG	
Sus1	(2217)	CTTCACAAAGTGCAGGGGAGGGGAGCCACTGGACCAAGATCTCCCAAGG	
Sus3	(2158)	CTTCGACCGGTCAGCAAGCAAGACCCAGATCACTGGTGATAATCTGGAG	
Consensus	(2251)	CTTCGACAAAGTGCAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG	
			2301
Sh1	(2287)	CGGGCCTGCAGAGAATTATGAGAAAGTACACCTGCAAGCTCACTCCGAG	
Sus1	(2267)	GGGGGCTCCAGCGTATCGAGGAGAAAGTACACCTGCAAGCTGACTCGGAG	
Sus3	(2208)	CAGGCTGCAGGCCATATAACAGAGAAGTACACATGGAAGATAACTCAGAG	
Consensus	(2301)	GCGGGCTGCAGCG AT TA GAGAAAGTACACCTGGAAGCT TACTC GAG	
			2350
Sh1	(2337)	AGGCTGATGACCCTGACCCGGTGTACGGGTCTCTGAAGTACGTGAGCA	
Sus1	(2317)	AGGCTGATGACCCCTACCCGGGTGTACGGGTCTCTGAAGTACGTGTCCAA	
Sus3	(2258)	AGGTGATGACACTGGCCGGGTCTACGGGTCTCTGAAGTACGTGTCGAA	
Consensus	(2351)	AGGCTGATGACCCTGACCCGGGTGTACGGGTCTCTGAAGTACGTGTCCAA	
			2400
Sh1	(2387)	CCTGGAGAGACCCGGAGACCCGCCGTAACATCCAGATCTCTACCCCTCA	
Sus1	(2367)	CCTGAGAGAGGCGAGACCCGGGTGTACCTGGAGATCTCTACCCCTCA	
Sus3	(2308)	GCTGGAGAGGCTGGAGAGGAGACCCGGCTACCTCACTGTTCTACATACTGA	
Consensus	(2401)	CCTGGAGAGGCGAGACCCGGCGCTACCT GAGATGTTCTACGC CTGA	
			2450
Sh1	(2437)	ACTACCGTAGGCTGCCAACCCAGGTCTGGCTGTCTCTCA-----TTAG	
Sus1	(2417)	ACTACCGCACCATGGGAGACCCGGGTGTACCTGGGUGTGCA-----GGCA	
Sus3	(2358)	ACTTCCGGAGGTGGGAAGACCCGTGGGCTTGTCAATTCACCAACCCGAG	
Consensus	(2451)	AGTACCGCA CCTGGCGAGCACCGTGGCGCTGGCCTGA ----- G AG	
			2500
Sh1	(2481)	TACGGGGAAAGAAGGAGA-AGAAGAACAGAAGAACCCAGGCCAGGCGGA-----G	
Sus1	(2461)	GAGCCCTCCAGCAACTGA-TGGCTGACGGCGCCACAGACCTGATC-----G	
Sus3	(2408)	TAGCTTGGCGCACTGCACTGGCTAGGACTTGGTACAAGACCTGAAACCTG	
Consensus	(2501)	TAGC GC AGAA G GA TGCGTAACA GGCACAGGCCTGA G	
			2550
Sh1	(2525)	AACCTTCGCGTGCATTTCGATCT-----GT-TTCACCCCAATTCGC	
Sus1	(2507)	ATGGCTGAGGGAGGGAGCACTCGGA-----GT-CTCGTGTCTTCTCC	
Sus3	(2458)	AGGCTCTTCACTAAATTAGGGCGGGCAGACGGTAGCCAATAAAATGIC	
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTGCG	
			2600
Sh1	(2565)	ATTGTTAGTGGGTATTGGAGTATGTG-----TACTGGTTCTCAAGAACCTT	
Sus1	(2551)	TTGCCATTCTCTCTCTCTCTCTCTCT-----TTCGGGAGGGCGAAAAAA	
Sus3	(2508)	CGGAGCTGAACGGTTGTTTAAATTATGACATAATGGCACTATAACAAAT	
Consensus	(2601)	TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT	
			2650
Sh1	(2613)	TGGCTCCTTCTCGTTTTTTCCTTCTTCTGAGGCTTTTGGCGAGCGCTG	
Sus1	(2599)	AGAGTC-TGCTT-TGCTAGGCCGCGGGCTTCTCTGCTCTCTTGCT	
Sus3	(2558)	TACTGAAGCTAGGCTGGGTGCACTTGTCTCTCTCTACTG-----T	
Consensus	(2651)	TG TTC TGCT GTTG CGTTGTTGTTCTG C G GCTT	
			2700
Sh1	(2663)	GCCCTGGTTCCTAGTATGGTGGGAATGGCTGCACCTTCTGCTTCAATAA	
Sus1	(2647)	CAAGAGTTAAATTCACCTACCT-----TCTGAGGTCTCTCTCCATCATTGA	
Sus3	(2600)	TACTGTATTATGTCAAGCTGCT-----GGCTGCAATTCTTGTCTGG-----CA	
Consensus	(2701)	ACTGGTT ATATTAAGCTG C TTGGCTGCA CTT TTC TGA T A	

Figure 9e

	2751	2800
Sh1	(2713) AAATGCCTGTCGGTTCACCTGTCTTCCAGAGTGC-----	
Sus1	(2695) TCCGGGTCTCGCTTGTAAGTACTCTGATGGACTGTAGTAGTGTTCGCGTTGC	
Sus3	(2644) AGCCGGAGGGACTGGTGAAAGTGGTGATAAAATACATATTCTGTTGACG	
Consensus	(2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C	
	2801	2850
Sh1	(2747) -----	
Sus1	(2745) GTCEGTTGAGAGGGAACGTTGGTGGTGGTGTGTGTCAAGTCAGGCCT	
Sus3	(2694) TGTAAAAAAAGGGCGGCCG-----	
Consensus	(2801) G A A AA G G G C	
	2851	2900
Sh1	(2747) -----	
Sus1	(2795) GGTGCTCCCTTGTTCCTGGATGGATGTTGCTCCTGAATAATAATCG	
Sus3	(2738) -----	
Consensus	(2851)	
	2901	2950
Sh1	(2747) -----	
Sus1	(2845) TAGTGGCCTTGGAGCCCTTCTGAAATAAGAGCAGCATCCTAGTGCTT	
Sus3	(2738) -----	
Consensus	(2901)	
	2951 2964	
Sh1	(2747) -----	
Sus1	(2895) ACCTTTGCAGCTGT	
Sus3	(2738) -----	
Consensus	(2951)	

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACTAGCCGCGGCCGGTAGGAG
CGCGCGCGCGCGGGAAACGACCCACCGGTGGCGGCAGCCATGTCTGCCCCGAAGCTGA
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCCTCACGCGACCGAACGAGC
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGACCACA
TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGTCCGCGCGCTCGCCGAGGGACCCT
TCCTCGACGTCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11

ATGTCGCCCGAACGCAACCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

atccaaaccac	gggtttccatcg	accgcgtcga	ggacacccctc	cacgcgcacc	gcaacgagct	60
cgtcgccctc	ctgtccaagt	acgtgaacaa	ggggaaaggc	atccctgcagc	cgcaccacat	120
cctcgacgctg	ctcgacgagg	tccagggtc	cggggccgc	gcgcgtccgg	agggaccctt	180
cctcgacgtc	ctccgctccg	cgcaggaggc	gatcgtgctg	ccgcgttccg	tggccatcg	240
ggtgcgcccc	cggccgggag	tttgggagta	cgtccgcgtc	aacgttcaecg	agctcagcgt	300
cgagcagctc	acagtctcg	agtacctccg	cttcaaggag	gagttgtcg	acggccagca	360
caatgatccc	tacgttctcg	agcttgactt	cgagccgttc	aatgtctcg	tcccacgccc	420
aaatccgtca	tcatctattt	gaaacgggt	gcagttccct	aaccgcacact	tgtcctcaat	480
catgttccgc	aacaggaggat	gcttggagcc	cctgttggat	ttcctccgtg	gccaccggca	540
caaggggcat	gttatgtatc	ttaatgatag	aatacaaagc	ttggggaggc	ttcagtctgt	600
gctgacaaa	gctgaggaggc	acttgtcaaa	gctccctgt	gacacacccat	actcacaatt	660
tgcttataaa	tttcaagagt	ggggccctgg	gaaagggtgg	ggtgatacag	caggacatgt	720
tttggaaatg	atccatctcc	ttcttagacat	cattcaggcg	ccagacccat	ctaccctaga	780
gaaattcttgc	gggaggatcc	ccatgat	ttacgttgg	gttgtatccc	ctcatggata	840
ctttggtaaa	gctaattgtat	taggcttgc	agacacagga	ggacagatcg	tctatatact	900
ggaccaagtc	cgtgcactag	aaaatgagat	ggttctccgt	ttaaagaaac	aagggcttga	960
tgtttcccca	aagattctca	ttgttactcg	gctgatacca	gatgcggaaa	gaacatcatg	1020
caatcagcgg	cttgagagaa	ttagtggaa	acagcatact	tacatattac	gagttccctt	1080
cagaaatgaa	aatgggatac	ttaagaatag	gatatacca	tttgcgtgt	ggccatatct	1140
gaaacacattt	gctgaggatg	ctgcttgg	aattgtctgt	gaattacaag	gtactccaga	1200
cttcataattt	ggaaactaca	gtgatggaaa	tcttgcgtcg	tcattgtct	ttacaagat	1260
gggatattacc	cagtgcaca	ttgctcatgc	tctggaaaag	actaagtatc	cagattcaga	1320
catattttgg	aagaatttcg	atgagaagta	ccatttctcc	tgccagtta	ctgctgat	1380
aattgttatg	aacaatgt	attttatcat	caccacaca	taccaagaaa	ttgcttggaa	1440
caaaaaatact	gttggacagt	atgagatca	tactgcctt	actctgcctg	gtctgtaccc	1500
agttgtccat	gggatcgatg	tcttcgtatcc	aaagttcaat	atagtctctc	ctggagctga	1560
catgtccata	tactttccac	ataccgagaa	ggccaagcga	ctcacctctc	ttcatggttc	1620
aatcgaaaat	ttgatattatg	accggagca	aaacgatgaa	cacattgggc	atctggatga	1680
ccggtaaaag	cccatccctc	tctccatggc	aagactcgac	agggtgaaga	acataacagg	1740
gctggtcgaa	gcttttgc	agtgcgtta	gctgaggagg	ctggtaaacc	ttgtcgtcg	1800
tgccgggtac	aatgtatgc	acaagtccaa	ggacaggaa	gagatcgcgg	agatagagaa	1860
gatgcgtatg	ctcatcaaga	cccacaactt	gttcggcag	ttccgttgg	tctctgccc	1920
gacaaacagg	gccccgtaa	gcgagctta	tcgtacatc	gtgtataccc	atggtgctt	1980
cgtacagccg	gccttgc	aagcgttccg	tctcaccgtc	gttgaggcca	tgacctgtgg	2040
gcttcctact	ttcggacgc	tccatggagg	tccagcttag	atcatagagc	atggcgttc	2100
gggcttccac	attgaccctgt	accacccca	acaggctgtt	aatctgtatgg	ccgacttctt	2160
cgaccgggtc	aagaacagacc	catatcactg	ggtgaatata	tctggaggcag	ggctgcagcg	2220
catatacgag	aagtacacat	ggaagatata	ctcagagagg	ttgatgacac	tggccggggt	2280
ctacgggttc	tggaaagtacg	tgtcgaagct	cgagggctg	gagacggggc	gctaccttga	2340
gatgttctac	atactgaatg	tccgcgtatc	ggcgaagacc	gtgcccgtt	caatttgcacca	2400
accgcgtatg	tttgcgttac	tcgtactcg	tagcattgg	tacaagactg	aaacctgaag	2460
gaccctcgt	attttaggcg	cggcagacgg	tagccaataa	aatgtccgg	agctgaactg	2520
gttttttattt	atgtatcaa	tggcgtatca	acaaaattac	tgaaggcagg	tgggttgcag	2580
ttgtgtgttc	gttactgtt	actgtattat	gtcaagtgt	cggtgtcaat	ttctttgtcg	2640
gcaagccgca	ggcactgtgt	aagtgtgtat	aaatacatca	tattctgtt	acctgtgaaa	2700
aaaaaaaaaa	aaaaaaaaaa	aaaaaaagg	cgccgc			

Figure 11